

SEQUENCE LISTING

1

<110> Lukyanov, Sergey

<120> FLUORESCENT PROTEINS FROM COPEPODA SPECIES AND METHODS FOR USING SAME

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<170> PatentIn version 3.1

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<212> PRT

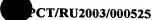
<213> Pontellina plumata

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Pro	Tvr		Leu	Ser	His	Val		Glv	የ የ	Glv	Phe		Hie	Phe	Glv
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Thr		Pro	Ser	Glv	Tyr		Asn	Pro	Phe	Len		Δla	Δla	Acn	Aen
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	Gly	ጥህ ዮ	ሞbr	Δen	Thr	Δrα	Tlo	Clu	T. 110		Clu	Λαν	C1	C1	
CLY	OLY	-7-	****	85	1111	Arg	116	Giu	90 50	тАт	Giu	rsp	GTĀ	95	vaı
Len	ui c	Wa l	802	• -	802	Tr	71	m		77.	C1	7	*** 7		G3
ъęч	nrs	VAI	100	rne	Ser	тАт	Arg	_	GIU	Ala	GTĀ	Arg		TTE	стА
7 000	Dh	T		T7 3	C1	m\	G1	105	D	6 7			110		_,
Asp	Pne		var	vaı	Gly	Inr		Pne	Pro	GIU	Asp		vaı	тте	Phe
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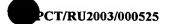
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<212> DNA

<213> Pontellina plumata

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65 70 75 80	
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85 90 95	
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly	
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115 120 125	
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130 135 140	
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145 150 155 160	
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165 170 175	
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe	
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<211> 814

<212> DNA

<213> Labidocera aestiva

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<210> 6

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Gly Gly Tyr Thr Asn Thr Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile 85 90 Ile Ser Val Asn Phe Thr Tyr Arg Tyr Glu Gly Asn Lys Val Ile Gly 100 Asp Phe Lys Val Val Gly Ser Gly Phe Pro Ala Asn Ser Val Ile Phe 120 125 Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro 135 140 Lys Gly Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu 145 150 155 160 Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Leu His Phe 165 170 Lys Thr Ala Met His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe 180 185 190 Thr Tyr Arg Lys Val Glu Glu Leu His Ser Gln Ser Asp Val Gly Ile 200 Val Glu Tyr Gln His Val Phe Lys Thr Pro Thr Ala Phe Ala 210 215 220

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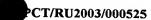
<213> cf. Pontella meadi Wheeler

<400> 7

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<210> 8

<211> 222



<212> PRT

<213> cf. Pontella meadi Wheeler

<400> 8

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<210> 9

<211> 880

210

<212> DNA

<213> cf. Pontella meadi Wheeler

215

<400> 9

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<210> 10

<211> 222

<212> PRT

<213> cf. Pontella meadi Wheeler

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 Lys
 Gly
 Gly
 Tyr
 Tyr
 Ser
 Ala
 Gln
 Val
 Asn
 Asn
 His
 Met
 His
 Phe

 Lys
 Ser
 Ala
 Ile
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 Pro
 Thr
 Met
 Leu
 Gln
 Asn
 Gly
 Ser
 Met
 Phe

 Lys
 Iso
 I

<210> 11 <211> 847

<212> DNA

<213> Pontella mediterranea

<400> 11

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<210> 12

<211> 222

<212> PRT

<213> Pontella mediterranea

<400> 12

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20 25 30



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3:		net hys	40	nys Gry			Pne	Ser
		Hie Val				45	_	
50	eu Leu Ser	55	nen GIA			Tyr His	Tyr	Ala
	ro Nia Ci.		B **- 1		60			
65	ro Ala Gly		Asn val		His .	Ala Met		
	_	70		75				80
GTA GTA L	yr Ser Asn	Thr Arg	Thr Glu		Glu .	Asp Gly	Gly	Ile
_	85			90			95	
Ile Ser A	la Thr Phe	Asn Tyr	Arg Tyr	Glu Gly	Arg	Gln Ile	His	Gly
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Asp Phe L	ys Val Val	Gly Thr	Gly Phe	Pro Ala	Asp	Ser Ile	Ile	Phe
1:	15		120			125		
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145		150		155				160
Arg Asp G	ly Gly Tyr	Tyr Ser	Ala Gln	Val Asn	Asn	His Met	His	Leu
	165			170			175	
Gln Ser A	la Ile His	Pro Thr	Met Leu	Lys Asn	Gly	Gly Ser	Met	Phe
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Thr Tyr A	rg Lys Val	Glu Glu	Leu His	Thr Gln	Thr	Glu Val	Glv	Ile
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<211> 850

<212> DNA

<213> Pontella mediterranea

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gcactcate cacaatgs agttggtatt gttgagtact agtagtgag gagttcatgt to cacaaatgg gagttgag gagttcatgt cacaaatga agtaggtgag gagttgag cacaactga agtaggtatt gttgagtact acaaataa agagttgag gagttgag cacaactgt cacaaatga to cacaaataa agagttgag tattattg tttctaaaacaaaaaaaaaa	gccatco	catc o	ccaco	catgo	et co	cagaa	ataat	. gga	atcta	atat	tcad	ectad	cag a	aaaa	attaaa
Second S															
Cally														_	
Second S															
Second Paragram Second Par															
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Are the control of the contr	1			5					10					15	
Arg Met Thr Ash Gln Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser Ser Thr Lys Gly Tyr Leu Gly Tyr Gly Tyr Tyr His Tyr Ala Sor Thr Sor Tyr Tyr Tyr His Tyr Ala Sor Tyr Tyr Tyr Tyr Ala Tyr Tyr Tyr Tyr Tyr Ala Tyr Tyr Tyr Tyr Tyr Ash Tyr Ty	Glu Gl	ı Phe	Glu	Leu	Val	Gly	Ala	Gly	Asp	Gly	Asn	Thr	Asp	Glu	Gly
Sample S			20					25					30		
Pro Tyr Leu Leu Ser His Val Leu Gly Tyr Tyr His Tyr Ala 50 55 55 55 60 50 50 55 60 55 60 55 60 55 60 60 55 80 60	Arg Me	t Thr	Asn	Gln	Met	Lys	Ser	Thr	Lys	Gly	Pro	Leu	Ser	Phe	Ser
So															
The Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Met Lys Asn 65		r Leu	Leu	Ser	His	Val	Leu	Gly	Tyr	Gly	Tyr	Tyr	His	Tyr	Ala
65															
Gly Gly Tyr Ser Asn Thr Arg Thr Glu Arg Tyr Asp Asp Gly Gly Ile 85		e Pro	Ala	Gly		Glu	Asn	Val	Tyr		His	Ala	Met	Lys	Asn
Ser Ala Thr Phe Asn Tyr Arg Tyr Glu Gly Arg Gln Ile His Gly		_													
The Ser Ala Thr Phe Ash Tyr Arg Tyr Glu Gly Arg Gln Ile His Gly	GIA GI	y Tyr	Ser		Thr	Arg	Thr	Glu		Tyr	Asp	Asp	Gly	Gly	Ile
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Ala Asp Ser Ile Ile Phe Ile Ile Phe Ile Ile Phe Ile Ile Ile Phe Ile Ile Ile Phe Ile Ile Ile Ile Phe Ile Ile Ile Ile Ile Ile Ile Ile Ile Il	T] - C-		573		_	_	_								
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Ala Asp Ser Ile Ile Phe 115	TTE SE	r Ala		Phe	Asn	Tyr	Arg		Glu	Gly	Arg	Gln		His	Gly
Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro 130	Aco Ph	. T		17 n 3	C1	m>	63		5		_	_			
Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro 130	Asp Ph		vaı	val	стА	Thr			Pro	ALA	Asp		Ile	Ile	Phe
130 135 140 Lys Ala Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu 145 150 155 155 160 Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn Asn His Met His Phe 165 160 170 175 175 Lys Ser Ala Ile His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe 180 185 190 190 190 Thr Tyr Arg Lys Val Glu Glu Leu His Thr Gln Thr Glu Val Gly Ile 195 200 205 205 Val Glu Tyr Gln His Val Phe Lys Arg Pro Thr Ala Phe Ala 140 140 140	ጥኮድ ለመ		Tla	Tla	T	C			m\	~	~ 1			_	
Lys Ala Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu 145			116	116	пуз		ASII	PLO	Thr	Cys		HIS	тте	туr	Pro
145			Asn	Tle	Len		Aen	Δla	Tree	Th.∽			П	Mak	T
Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Phe 165		ор	11011			Val	ASII	ALG	TAT		ALG	1111	irb	Met	
Lys Ser Ala Ile His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe 180		o Glv	Glv	Tvr		Ser	Αla	Gln	Val		Aen	ніс	Mot	uic	
Lys Ser Ala Ile His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe 180	. 5	1	~ - 3		- 3 -					11011	11011	1143	1766		EHG
Thr Tyr Arg Lys Val Glu Glu Leu His Thr Gln Thr Glu Val Gly Ile 195 200 205 Val Glu Tyr Gln His Val Phe Lys Arg Pro Thr Ala Phe Ala	Lys Se	r Ala	Ile		Pro	Thr	Met	Len		Asn	Glv	G1 ហ	Ser		Phe
Thr Tyr Arg Lys Val Glu Glu Leu His Thr Gln Thr Glu Val Gly Ile 195 200 205 Val Glu Tyr Gln His Val Phe Lys Arg Pro Thr Ala Phe Ala	_					-					y	~ - y		ムムじし	F 11G
195 200 205 Val Glu Tyr Gln His Val Phe Lys Arg Pro Thr Ala Phe Ala	Thr Ty	r Arg		Val	Glu	Glu	Leu		Thr	Gln	Thr	Glu		G] v	Ile
Val Glu Tyr Gln His Val Phe Lys Arg Pro Thr Ala Phe Ala	_		-											-+1	-20
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nec Ai	a Ala Met Lys 5	rie Giu Cys		GIY THE ME	_								
		val Clu Clu	10	Non Mhw No	15								
•a1 G1	u Phe Glu Leu 20		ery eru ery 25	Asn Thr As	о ети етА								
Ara Me	et Thr Asn Lys				r Dha Sor								
9 *10	35	40	mys Gry	45	r the per								
Pro Tv	r Leu Leu Ser		Glv Tvr Glv		s Phe Glv								
- 4													

55 ·

Thr Phe Pro Ser Gly Tyr Glu Asn Pro Tyr Val His Ala Met Thr Asn	
65 70 75 80	
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Ser Tyr Glu Asp Gly Gly Val 85 90 95	
85 90 95 Leu Tyr Leu Thr Phe Asn Tyr Arg Leu Asp Gly Asn Lys Ile Ile Gly	
100 105 110 Asp Phe Lys Cys Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe	
115 120 125	
Thr Asp Lys Ile Ile Lys Ser Asn Pro Asn Cys Glu His Phe Tyr Pro	
130 135 140	
Met Ala Glu Asn Ile Met Lys Asn Ala Tyr Met Arg Thr Leu Ser Leu	
145 150 155 160	
Arg Asp Gly Gly Tyr Tyr Ser Gly Gln Val Thr Ser His Ile His Phe	
165 170 175	
Lys Asn Ala Ile His Pro Ser Ile Leu His Asn Gly Gly Ser Met Phe	
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Thr Tyr Arg Arg Val Glu Glu Leu His Thr Gln Thr Asp Leu Gly Ile	
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210 215 220	
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accaagggcg ccctgacctt cagcccctac ctgctgagcc acgtgatggg ctacggcttc	180
taccacttcg gcacctaccc cageggctac gagaacccct teetgcaege cateaacaac	240
ggcggctaca ccaacacccg catcgagaag tacgaggacg gcggcgtgct gcacgtgagc	300
ttcagctacc gctacgaggc cggccgcgtg atcggcgact tcaaggtggt gggcaccggc	360
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cgcgacggcg gctactacag cttcgtggtg gacagccaca tgcacttcaa gagcgccatc	540
caccccagca tectgeagaa egggggeeee atgttegeet teegeegegt ggaggagetg	600
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<210> 19

<211> 589

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<212> DNA

<213> Artificial sequence

215



<220>

<223> nucleic acid sequence for the ppluGFP2 with yeast-optimized codon

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aattgaaaaa	tatgaagatg	gtggtgtttt	gcatgtttct	ttttcttata	gatatgaagc	240
tggtagagtt	attggcgatt	ttaaagttgt	tggtactggt	tttccagaag	attctgttat	300
ttttactgat	aaaattatta	gatctaatgc	tactgttgaa	catttgcatc	caatgggtga	360
taatgttttg	gttggttctt	ttgctagaac	tttttctttg	agagatggtg	gttattattc	420
ttttgttgtt	gattctcata	tgcattttaa	atctgctatt	catccatcta	ttttgcaaaa	480
tggtggtcca	atgtttgctt	ttagaagagt	tgaagaattg	cattctaata	ctgaattggg	540
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<210> 20

<211> 222

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the ppluGFP2 with yeast-optimized codon u sage

<400> 20

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105

Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe 120 125



Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro 135 140 Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu 150 155 Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe 165 170 Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe 180 185 Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile 195 200 205 Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala 210 215 220

<210> 21

<211> 669

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the CopCFP mutant

<400> 21

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<210> 22

<211> 222

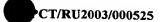
<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the CopCFP mutant

<400> 22



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Val Glu Phe Glu Leu Val Gly Gly Glu Gly Thr Pro Glu Gln Gly
20 25 30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
35 40 45
Pro Tyr Leu Leu Ser His Val Met Gly Trp Gly Phe Tyr His Phe Gly 50 55 60
50 55 60 Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65 70 75 80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
85 90 95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
100 105 110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
115 120 125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu Arg Pro
130 135 140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145 150 155 160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe 165 170 175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
180 185 190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
195 200 205.
Val Glu Tyr Gln His Ala Phe Lys Thr Pro Thr Ala Phe Ala
210 215 220
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<211> 690 <212> DNA
<213> Artificial sequence
<220>
<223> nucleic acid sequence for the CopGFP-NA1 variant
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atgaccaaca agatgaagag caccaagggc gccctgacct tcagccccta cctgctgagc
Cacataataa actacaaatt ataaaaatta aaaaatta

cacgtgatgg gctacggctt ctaccacttc ggcacctacc ccagcggcta cgagaacccc



540 ·

ttcctgcacg ccatcaacaa cggcggctac accaacacc gcatcgagaa gtacgaggac												
ggcggcgtgc tgcacgtgag cttcagctac cgctacgagg ccggccgcgt gatcggcgac												
ttcaaggtgg tgggcaccgg cttccccgag gacagcgtga tcttcaccga caagatcatc												
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<213> Artificial sequence												
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20 25 30												
Glu Gly Thr Pro Glu Gln Gly Arg Met Thr Asn Lys Met Lys Ser Thr												
. 35 40 45												
Lys Gly Ala Leu Thr Phe Ser Pro Tyr Leu Leu Ser His Val Met Gly												
50 55 60												
Tyr Gly Phe Tyr His Phe Gly Thr Tyr Pro Ser Gly Tyr Glu Asn Pro												
65 70 75 80												
Phe Leu His Ala Ile Asn Asn Gly Gly Tyr Thr Asn Thr Arg Ile Glu												
85												
Lys Tyr Glu Asp Gly Gly Val Leu His Val Ser Phe Ser Tyr Arg Tyr												
100 105 110												
Glu Ala Gly Arg Val Ile Gly Asp Phe Lys Val Val Gly Thr Gly Phe												
115 120 125												
Pro Glu Asp Ser Val Ile Phe Thr Asp Lys Ile Ile Arg Ser Asn Ala												
130 135 140												
Thr Val Glu His Leu His Pro Met Gly Asp Asn Val Leu Val Gly Ser												
145 150 155 160												
Phe Ala Arg Thr Phe Ser Leu Arg Asp Gly Gly Tyr Tyr Ser Phe Val												
165 170 175												
Val Asp Ser His Met His Phe Lys Ser Ala Ile His Pro Ser Ile Leu												
180 185 190												



Gln Asn Gly Gly Pro Met Phe Ala Phe Arg Arg Val Glu Glu Leu His
195
200
205
Ser Asn Thr Glu Leu Gly lie Val Glu Tyr Gln His Ala Phe Lys Thr
210
215
220

Pro Ile Ala Phe Ala

225

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<211> 819

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the CopGFP-NA2 variant

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<211> 272

<212> PRT

<213> Artificial sequence

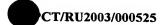
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<223> amino acid sequence for the CopGFP-NA2 variant

<400> 26

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1 5 10 15



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<210> 27

<211> 840

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the CopGFP-NA3 variant

<400> 27

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cacgtgatgg	gctacggctt	ctaccacttc	ggcacctacc	ccagcggcta	cgagaacccc	240
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ttcaaggtgg	tgggcaccgg	cttccccgag	gacagcgtga	tcttcaccga	caagatcatc	420
cgcagcaacg	ccaccgtgga	gcacctgcac	cccatgggcg	ataacgtgct	ggtgggcagc	480
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ttccgccgcg	tggaggagct	gcacagcaac	accgagctgg	gcatcgtgga	gtaccagcac	660
gccttcaaga	ccccgatcgc	attcgccaga	tccagagccc	aggccagcaa	ctccgccgtg	720
gatggcacag	ccggaccggg	atcggccgcg	actctagatc	ataatcagcc	ataccacatt	780
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<211> 279

<212> PRT

<213> Artificial sequence

<220>

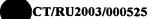
<223> amino acid sequence for the CopGFP-NA3 variant

<400> 28

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140



Thr	Val	Glu	His	Leu	His	Pro	Met	${\tt Gly}$	Asp	Asn	Val	Leu	Val	Gly	Ser
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Phe	Ala	Arg	Thr	Phe	Ser	Leu	Arg	Asp	Gly	Gly	Tyr	Tyr	Ser	Phe	Val
				165					170					175	
Val	Asp	Ser	His	Met	His	Phe	Lys	Ser	Ala	Ile	His	Pro	Ser	Ile	Leu
			180					185					190		
Gln	Asn	Gly	Gly	Pro	Met	Phe	Ala	Phe	Arg	Arg	Val	Glu	Glu	Leu	His
		195					200					205			
Ser	Asn	Thr	Glu	Leu	Gly	Ile	Val	Glu	Tyr	Gln	His	Ala	Phe	Lys	Thr
	210					215					220				
Pro	Ile	Ala	Phe	Ala	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Asn	Ser	Ala	Val
225					230					235					240
Asp	Gly	Thr	Ala	Gly	Pro	Gly	Ser	Ala	Ala	Thr	Leu	Asp	His	Asn	Gln
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Pro	Tyr	His	Ile	Cys	Arg	Gly	Phe	Thr	Cys	Phe	Lys	Lys	Pro	Pro	Thr
			260					265	•				270		
Pro	Pro	Pro	Glu	Pro	Glu	Thr									
		275													